



1646

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/780,576

DATE: 01/28/2002

TIME: 18:01:05

Input Set : A:\Uc4530.txt

Output Set: N:\CRF3\01282002\I780576.raw

ENTERED

Paper M...

Mar 3, 2002

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4 <110> APPLICANT: Civelli, Olivier
5      Nothacker, Hans-Peter
6      Wang, Zhiwei
7      Reinscheid, Rainer
9 <120> TITLE OF INVENTION: ADP-Glucose Receptor
12 <130> FILE REFERENCE: P-UC 4530
14 <140> CURRENT APPLICATION NUMBER: US 09/780,576
15 <141> CURRENT FILING DATE: 2001-02-09
17 <150> PRIOR APPLICATION NUMBER: US 60/234,025
18 <151> PRIOR FILING DATE: 2000-09-20
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1143
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (52)...(1077)
33 <400> SEQUENCE: 1
34 taggctgaaa ataaccatcc tctcttttgt tctctaggta accaacaaga a atg caa 57
35                                     Met Gln
36                                     1
38 gcc gtc gac aac ctc acc tct gcg cct ggt aac acc agt ctg tgc acc 105
39 Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr
40      5              10              15
42 aga gac tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc 153
43 Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val
44      20              25              30
46 ctg ttt ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc 201
47 Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe
48 35              40              45              50
50 ttt caa atc cgg agt aaa tca aac ttt att att ttt ctt aag aac aca 249
51 Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr
52      55              60              65
54 gtc att tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt 297
55 Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu
56      70              75              80
58 agt gat gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa 345
59 Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln
60      85              90              95
62 gtt acc tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc 393
63 Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe

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64      100      105      110
66 ctg gga ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt 441
67 Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe
68 115      120      125      130
70 aaa aca tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc tct gtt 489
71 Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val
72      135      140      145
74 gtc atc tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg 537
75 Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu
76      150      155      160
78 acc aac agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt 585
79 Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu
80      165      170      175
82 aaa tca gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt 633
83 Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys
84      180      185      190
86 caa gtc att ttc tgg att aat ttc tta att gtt att gta tgt tat aca 681
87 Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr
88 195      200      205      210
90 ctc att aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta 729
91 Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val
92      215      220      225
94 ggt aaa gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att 777
95 Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ile
96      230      235      240
98 gct gta ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct 825
99 Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro
100      245      250      255
102 tac acc ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat 873
103 Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn
104      260      265      270
106 act ctg ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat 921
107 Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn
108 275      280      285      290
110 gca tgc ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga 969
111 Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg
112      295      300      305
114 aat tcc ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg 1017
115 Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu
116      310      315      320
118 tcc cag gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa 1065
119 Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu
120      325      330      335
122 gag act cca atg taaacaaatt aactaaggaa atatttcaat ctctttgtgt 1117
123 Glu Thr Pro Met
124      340
126 tcagaactcg ttaaagcaaaa gcgcta 1143
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 342

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130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
134 Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
135 1 5 10 15
136 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
137 20 25 30
138 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
139 35 40 45
140 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
141 50 55 60
142 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
143 65 70 75 80
144 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
145 85 90 95
146 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
147 100 105 110
148 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
149 115 120 125
150 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
151 130 135 140
152 Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
153 145 150 155 160
154 Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
155 165 170 175
156 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
157 180 185 190
158 Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
159 195 200 205
160 Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
161 210 215 220
162 Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
163 225 230 235 240
164 Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
165 245 250 255
166 Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
167 260 265 270
168 Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
169 275 280 285
170 Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
171 290 295 300
172 Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
173 305 310 315 320
174 Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
175 325 330 335
176 Asn Glu Glu Thr Pro Met
177 340
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 24

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Input Set : A:\Uc4530.txt

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182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: synthetic primer
188 <400> SEQUENCE: 3
189 atggagggga agctagagaa gagt 24
191 <210> SEQ ID NO: 4
192 <211> LENGTH: 23
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: synthetic primer
199 <400> SEQUENCE: 4
200 tagcgccttg cttaaagag ttc 23
202 <210> SEQ ID NO: 5
203 <211> LENGTH: 34
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: synthetic primer
210 <400> SEQUENCE: 5
211 actgaagctt taggctgaaa ataaccatcc tctc 34
213 <210> SEQ ID NO: 6
214 <211> LENGTH: 32
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: synthetic primer
221 <400> SEQUENCE: 6
222 cgactcgagt agcgccttgc ttaaagag ttc 32

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/780,576

DATE: 01/28/2002

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Input Set : A:\Uc4530.txt

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